Full wwPDB X-ray Structure Validation Report (i)

May 29, 2024 – 06:53 PM EDT

PDB ID	:	1TNG
Title	:	PREDICTION OF NOVEL SERINE PROTEASE INHIBITORS
Authors	:	Kurinov, I.; Harrison, R.W.
Deposited on	:	1994-07-21
Resolution	:	1.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the (i) symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

The following versions of software and data (see references (i)) were used in the production of this report:

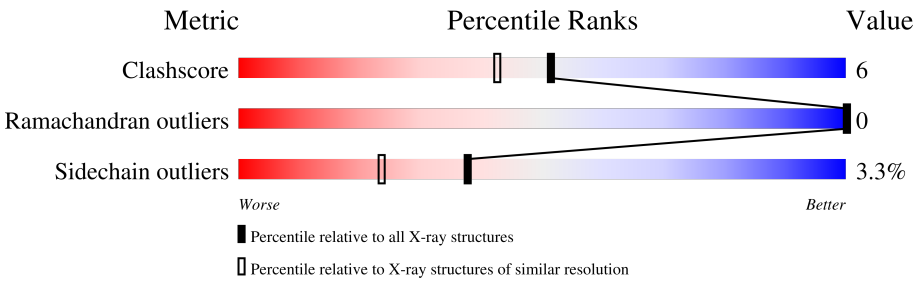
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	229	81% 15% • •

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 2512 atoms, of which 711 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

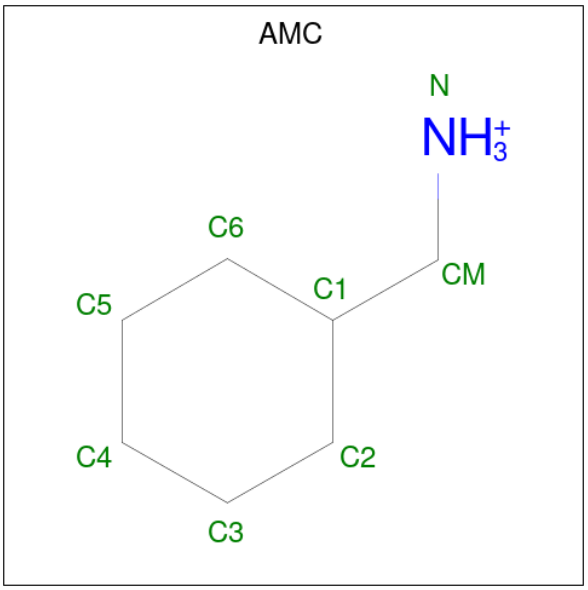
- Molecule 1 is a protein called TRYPSIN.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	H	N	O	S			
1	A	223	2011	1012	382	279	324	14	0	0	0

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Ca		
2	A	1	1	1	0	0

- Molecule 3 is AMINOMETHYLCYCLOHEXANE (three-letter code: AMC) (formula: $C_7H_{16}N$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	H	N		
3	A	1	11	7	3	1	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	H	O		
4	A	163	489	326	163	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

Note EDS was not executed.

• Molecule 1: TRYPSIN

Chain A:

4 Data and refinement statistics (i)

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	54.95Å 58.42Å 67.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	7.00 – 1.80	Depositor
% Data completeness (in resolution range)	(Not available) (7.00-1.80)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.172 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	2512	wwPDB-VP
Average B, all atoms ($Å^2$)	17.0	wwPDB-VP

5 Model quality (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: AMC, CA

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\#\|Z\|>5$	RMSZ	$\#\|Z\|>5$
1	A	0.79	0/1660	1.50	21/2250 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

There are no bond length outliers.

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	141	TRP	CD1-CG-CD2	8.40	113.02	106.30
1	A	237	TRP	CD1-CG-CD2	7.88	112.60	106.30
1	A	141	TRP	CE2-CD2-CG	-7.80	101.06	107.30
1	A	51	TRP	CD1-CG-CD2	7.15	112.02	106.30
1	A	215	TRP	CD1-CG-CD2	7.02	111.92	106.30
1	A	240	GLN	CA-CB-CG	6.91	128.59	113.40
1	A	237	TRP	CE2-CD2-CG	-6.90	101.78	107.30
1	A	51	TRP	CE2-CD2-CG	-6.60	102.02	107.30
1	A	215	TRP	CE2-CD2-CG	-6.19	102.35	107.30
1	A	237	TRP	CG-CD2-CE3	6.05	139.34	133.90
1	A	210	GLN	OE1-CD-NE2	-5.98	108.15	121.90
1	A	210	GLN	CG-CD-NE2	5.84	130.71	116.70
1	A	117	ARG	NE-CZ-NH2	-5.77	117.41	120.30
1	A	237	TRP	CG-CD1-NE1	-5.73	104.37	110.10
1	A	151	TYR	CB-CG-CD1	-5.41	117.75	121.00
1	A	240	GLN	N-CA-CB	-5.35	100.96	110.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	215	TRP	CG-CD1-NE1	-5.35	104.75	110.10
1	A	51	TRP	CG-CD2-CE3	5.21	138.59	133.90
1	A	141	TRP	CB-CG-CD1	-5.20	120.24	127.00
1	A	141	TRP	CG-CD2-CE3	5.15	138.53	133.90
1	A	72	ASN	OD1-CG-ND2	-5.05	110.27	121.90

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	59	TYR	Sidechain

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	1629	382	1588	17	0
2	A	1	0	0	0	0
3	A	8	3	16	0	0
4	A	163	326	0	1	0
All	All	1801	711	1604	17	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 6.

All (17) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:72:ASN:HD22	1:A:74:ASN:H	1.32	0.76
1:A:34:ASN:ND2	1:A:38:GLY:H	1.97	0.62
1:A:64:GLN:NE2	1:A:66:ARG:HE	1.98	0.61
1:A:138:ILE:HG12	1:A:199:VAL:HG22	1.83	0.60
1:A:72:ASN:ND2	1:A:74:ASN:H	2.03	0.55
1:A:45:SER:OG	1:A:198:PRO:HB3	2.08	0.53
1:A:72:ASN:HD22	1:A:74:ASN:N	2.05	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86:SER:HB3	1:A:109:LYS:HG2	1.93	0.50
1:A:64:GLN:HE22	1:A:66:ARG:HH21	1.58	0.49
1:A:31:VAL:HG12	1:A:67:LEU:HD23	1.98	0.44
1:A:87:LYS:HD3	1:A:89:ILE:HD11	2.00	0.43
1:A:145:LYS:HE2	1:A:145:LYS:HA	2.01	0.43
1:A:192:GLN:HB3	4:A:407:HOH:O	2.20	0.42
1:A:135:GLN:HG2	1:A:136:CYS:N	2.35	0.41
1:A:221:GLN:HB2	1:A:224:LYS:HB2	2.01	0.41
1:A:29:TYR:CZ	1:A:200:VAL:HG21	2.56	0.41
1:A:56:ALA:HB1	1:A:90:VAL:HG13	2.04	0.40

There are no symmetry-related clashes.

5.3 Torsion angles (i)

5.3.1 Protein backbone (i)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	221/229 (96%)	217 (98%)	4 (2%)	0	100 100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	184/190 (97%)	178 (97%)	6 (3%)	38 23

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72	ASN
1	A	99	LEU
1	A	145	LYS
1	A	185	LEU
1	A	186	GLU
1	A	192	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	34	ASN
1	A	64	GLN
1	A	72	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
3	AMC	A	900	-	8,8,8	0.61	0	8,9,9	0.77	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	AMC	A	900	-	-	0/2/10/10	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains (i)

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.